


SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Grotendorst, Gary R.
Bradham Jr., Douglas M.,

5 (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 2

10 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Spensley Horn Jubas & Lubitz
(B) STREET: 4225 Executive Square, Suite 1400
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 92037

15 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

20 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 30-AUG-1991
(C) CLASSIFICATION:

25 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wetherell, Jr. Ph.D., John W.
(B) REGISTRATION NUMBER: 31,678
(C) REFERENCE/DOCKET NUMBER: PD-1294

30 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-455-5100
(B) TELEFAX: 619-455-5110



(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
 (B) TYPE: nucleic acid
 5 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: DB60R32

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
 ~~~ (B) LOCATION: 130..1177

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|    |                                                                   |     |
|----|-------------------------------------------------------------------|-----|
|    | CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG | 60  |
| 15 | CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA | 120 |
|    | GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC     | 168 |
|    | Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe               |     |
|    | 1 5 10                                                            |     |
| 20 | GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC   | 216 |
|    | Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys   |     |
|    | 15 20 25                                                          |     |
|    | AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG   | 264 |
|    | Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala   |     |
|    | 30 35 40 45                                                       |     |
| 25 | GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC   | 312 |
|    | Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala   |     |
|    | 50 55 60                                                          |     |
|    | AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC   | 360 |
| 30 | Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His   |     |
|    | 65 70 75                                                          |     |

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|    |                                                                 |     |
|----|-----------------------------------------------------------------|-----|
|    | AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC | 408 |
|    | Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly |     |
|    | 80 85 90                                                        |     |
| 5  | GTG TGC ACC GCC AAA GAT GGT GCT CCC TGC ATC TTC GGT GGT ACG GTG | 456 |
|    | Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val |     |
|    | 95 100 105                                                      |     |
|    | TAC CGC AGC GGA GAG TCC TTC CAG AGC AGC TGC AAG TAC CAG TGC ACG | 504 |
|    | Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr |     |
|    | 110 115 120 125                                                 |     |
| 10 | TGC CTG GAC GGG GCG GTG GGC TGC ATG CCC CTG TGC AGC ATG GAC GTT | 552 |
|    | Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val |     |
|    | 130 135 140                                                     |     |
| 15 | CGT CTG CCC AGC CCT GAC TGC CCC TTC CCG AGG AGG GTC AAG CTG CCC | 600 |
|    | Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro |     |
|    | 145 150 155                                                     |     |
|    | GGG AAA TGC TGC GAG GAG TGG GTG TGT GAC GAG CCC AAG GAC CAA ACC | 648 |
|    | Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr |     |
|    | 160 165 170                                                     |     |
| 20 | GTG GTT GGG CCT GCC CTC GCG GCT TAC CGA CTG GAA GAC ACG TTT GGC | 696 |
|    | Val Val Gly Pro Ala Leu Ala Tyr Arg Leu Glu Asp Thr Phe Gly     |     |
|    | 175 180 185                                                     |     |
|    | CCA GAC CCA ACT ATG ATT AGA GCC AAC TGC CTG GTC CAG ACC ACA GAG | 744 |
|    | Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu |     |
|    | 190 195 200 205                                                 |     |
| 25 | TGG AGC GCC TGT TCC AAG ACC TGT GGG ATG GGC ATC TCC ACC CGG GTT | 792 |
|    | Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val |     |
|    | 210 215 220                                                     |     |
| 30 | ACC AAT GAC AAC GCC TCC TGC AGG CTA GAG AAG CAG ACC CGC CTG TGC | 840 |
|    | Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys |     |
|    | 225 230 235                                                     |     |
|    | ATG GTC AGG CCT TGC GAA GCT GAC CTG GAA GAG AAC ATT AAG AAG GGC | 888 |
|    | Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly |     |
|    | 240 245 250                                                     |     |

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|    |                                                                                                                                                                                                                                                                                                                                                                                                                          |                               |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------|
|    | AAA AAG TGC ATC CGT ACT CCC AAA ATC TCC AAG CCT ATC AAG TTT GAG<br>Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu<br>255 260 265                                                                                                                                                                                                                                                                        | 936                           |
| 5  | CCT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA<br>Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly<br>270 275 280 285                                                                                                                                                                                                                                                                    | 984                           |
|    | GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG<br>Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu<br>290 295 300                                                                                                                                                                                                                                                                            | 1032                          |
| 10 | CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAC ATG<br>Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met<br>305 310 315                                                                                                                                                                                                                                                                            | 1080                          |
| 15 | ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT<br>Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn<br>320 325 330                                                                                                                                                                                                                                                                        | 1128                          |
|    | GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T<br>Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala<br>335 340 345                                                                                                                                                                                                                                                                      | 1177                          |
| 20 | GAAGCCAGAG AGTGAGAGAC ATTAACATCAT TAGACTGGAA CTTGAACATGA TTACACATCTC<br>ATTTTCGGT AAAATGATT TCAGTAGCAC AAGTTATTAA AATCTGTTT TCTAACTGGG<br>GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC<br>CCAGACACTG GTTGAAGAA TGTAAAGACT TGACAGTGGAA ACTACATTAG TACACAGCAC<br>CAGAATGTAT ATTAAGGTGT GGCTTAGGA GCAGTGGAG GGTACCGGCC CGGTTAGTAT<br>CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATT GAAGTGTAAAT TGAGAAGGAA | 1237 1297 1357 1417 1477 1537 |
| 25 | AATTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC<br>CAGCCATCAA GAGACTGAGT CAAGTTGTT CTTAAGTCAG AACAGCAGAC TCAGCTCTGA<br>CATTCTGATT CGAATGACAC TGTTCAAGGAA TCGGAATCCT GTGGATTAGA CTGGACAGCT<br>TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTA AAATTTATAT TGTAAATATT<br>GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTAA                                                                       | 1597 1657 1717 1777 1837      |



|                                                                  |      |
|------------------------------------------------------------------|------|
| AGTTGTTTGT GCCTTTTAT TTTTGTTTT AATGCTTGA TATTCAATG TTAGCCTCAA    | 1897 |
| TITCTGAACA CCATAGGTAG AATGTAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT | 1957 |
| ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTGGCAAA | 2017 |
| GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG  | 2075 |

## 5 (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

10 ... (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|                                                                 |   |    |    |
|-----------------------------------------------------------------|---|----|----|
| Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu |   |    |    |
| 1                                                               | 5 | 10 | 15 |

|                                                                 |    |    |  |
|-----------------------------------------------------------------|----|----|--|
| Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro |    |    |  |
| 20                                                              | 25 | 30 |  |

|                                                                 |    |    |  |
|-----------------------------------------------------------------|----|----|--|
| Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser |    |    |  |
| 35                                                              | 40 | 45 |  |

|                                                             |    |    |  |
|-------------------------------------------------------------|----|----|--|
| Leu Val Leu Asp Gly Cys Gly Cys Arg Val Cys Ala Lys Gln Leu |    |    |  |
| 50                                                          | 55 | 60 |  |

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu |    |    |    |
| 65                                                              | 70 | 75 | 80 |

|                                                                 |    |    |  |
|-----------------------------------------------------------------|----|----|--|
| Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr |    |    |  |
| 85                                                              | 90 | 95 |  |

|                                                                 |     |     |  |
|-----------------------------------------------------------------|-----|-----|--|
| Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser |     |     |  |
| 100                                                             | 105 | 110 |  |

|                                                                 |     |     |  |
|-----------------------------------------------------------------|-----|-----|--|
| Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp |     |     |  |
| 115                                                             | 120 | 125 |  |

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Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro  
130 135 140

Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys  
145 150 155 160

5 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly  
165 170 175

Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro  
180 185 190

Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala  
10 195 200 205

Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp  
210 215 220

Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg  
225 230 235 240

15 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Cys  
245 250 255

Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly  
260 265 270

20 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr  
275 280 285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu  
290 295 300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile  
305 310 315 320

25 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe  
325 330 335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
340 345

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